

## SEQUENCE LISTING

&lt;110&gt; FMC Corporation

Wu, Shilan

Allenza, Paul

Halling, Blaik

&lt;120&gt; Aphis gossypii Polo-like Kinases

&lt;130&gt; 60294

&lt;160&gt; 9

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 2240

&lt;212&gt; DNA

&lt;213&gt; Aphis gossypii

&lt;400&gt; 1

aaagctcctc tgaacgtcgc aacggctaaa tcgtattacg ttacggttct gcgtttttaa	60
attcctttgt taacgtatac tttttgccga tcaacacggg agttactagt cagtgtacaa	120
ttgttaattg tcggcgggtga tcgttgagtc cgtgggtgcc acttgtccta taaatcctaa	180
gttctaccgt caacagccaa catgtcgtct agaccaaag aagaagaagt ccgaatccc	240
gacgtgattt tcgacaacaa gaccaacaag aagtatcaa aaggcagttt tctcggaaag	300
ggagggtttg caaatgtta tgaaattggt gatttgaaaa cttaaagaaat ctttgctgga	360
aaaattggtt ccaaaaaata tctattgaaa cacaaccaa aagataaaat gacacaagaa	420
atacatattc acaagatggt gaaacatata aacattgtta cttttcatag tttctttgag	480
gataatgact ttgtttatat tgttttggaa ctttgccgga aaagatcaat gatggagctg	540
cataagagaa gaaaaactct tactgaaccc gaaacacgtt actacgtatt tcaaattctt	600
gaagggacat tatatttaca taatcagggt attattcatc gtgatctgaa attaggaaat	660

ctatTTTTaa atgatgaaat ggaagtgaag ataggagatt tgggtttggc tgctagaatt 720  
gaatatgatg gacaacgtaa aaaaacatta tgtggcactc caaattatat tgctccagag 780  
attcttagca agactgggtca cagttttgaa gttgatgttt ggtccattgg ttgtataatg 840  
tacacactat tagttggcaa accaccattt gagacaaact ctctgaaaga aacatatgct 900  
aggattgcac gatgtgatta tagcttacca cctcatttaa ataagaatgc tagttcatta 960  
attaataaaa tgcttcaata tgatcctaaa aaacgtcctt gtgtatctga tataatgaaa 1020  
gctgatttct ttactactgg ttatatgcct aaaaaattac ctccatcatg tcttacaatg 1080  
gctcctcggt ttgattctat caattacaga gaatcaattt ctaatcgag accactcaat 1140  
gaactcaata gcccacaaagc tgccatcatt aaagttgctt ctaaacctca agatccggtt 1200  
aataaattgc caatgtttaa tattccaaat aaaccaacta ctggaaatgg tgtttcatcc 1260  
aatgactgta aagaatacat gatgtccctt gaaagagaat tgggaaattt attgaaatgt 1320  
aaaccaacca tgaaaggaat gaaaaacatg gagggaaaaca ctgaccagc tgctcaacct 1380  
ctcatttggg ttagtaaattg ggtggactat tccgataaat atggatttgg atatgaatta 1440  
tctgatgatt gtgttggtgt tatgttcaat gattttacca gaatagtact tttagccaat 1500  
ctaaaagatg tccattacat agaaagaaat ggttcagaac aataccatac aactgaacat 1560  
actccaccgt cgtagagaa aaaaatgaag ttattgatgt acttcagacg ttacatgaat 1620  
gatcatotta ttaaagctgg tgctgatata ttagctaaag atgcagacca attgagtcgt 1680  
acaccatata tgtaccaatg gtataggtct acttcatcag ttattatgca acttactaac 1740  
ggcactttac aaatcaactt cacagatcat acaaaagtaa tattgtgtcc attaataaat 1800  
gctgtcacct ttattgaaaa taatgttttc cgtacatacc gttttaatac aattgctgaa 1860  
catggctgta gccctgaatt aggaaaatgc ttggaatatg ctcaacagaa aattggatct 1920  
atattaaaag atagcccagt ttaatttact tgaaaattga cgagtatatt tagtttatag 1980

ttatgataat taatgaaaaa ccagtactta tgttaaaaga gctatattta agattgtaaa 2040  
 taattactat tattttttttt atttttacaat attaataatta aaccttaaaa ttaaatagtt 2100  
 tcatttatta ttattttttat tattttctatt ttgtgatttt tgttatttag aaaactatta 2160  
 tttcatcaaa ataaagtgac ttaagtacat ttagttacat attaaaaaat ctaatatgtt 2220  
 tttccatggg tgcattaaaa 2240

<210> 2  
 <211> 580  
 <212> PRT  
 <213> Aphis gossypii

<400> 2

Met Ser Ser Arg Pro Lys Glu Glu Glu Val Arg Ile Pro Asp Val Ile  
 1 5 10 15

Phe Asp Asn Lys Thr Asn Lys Lys Tyr Gln Lys Gly Ser Phe Leu Gly  
 20 25 30

Lys Gly Gly Phe Ala Lys Cys Tyr Glu Ile Val Asp Leu Lys Thr Lys  
 35 40 45

Glu Ile Phe Ala Gly Lys Ile Val Ser Lys Lys Tyr Leu Leu Lys His  
 50 55 60

Asn Gln Lys Asp Lys Met Thr Gln Glu Ile His Ile His Lys Met Leu  
 65 70 75 80

Lys His Thr Asn Ile Val Thr Phe His Ser Phe Phe Glu Asp Asn Asp  
 85 90 95

Phe Val Tyr Ile Val Leu Glu Leu Cys Arg Lys Arg Ser Met Met Glu  
100 105 110

Leu His Lys Arg Arg Lys Thr Leu Thr Glu Pro Glu Thr Arg Tyr Tyr  
115 120 125

Val Phe Gln Ile Leu Glu Gly Thr Leu Tyr Leu His Asn Gln Gly Ile  
130 135 140

Ile His Arg Asp Leu Lys Leu Gly Asn Leu Phe Leu Asn Asp Glu Met  
145 150 155 160

Glu Val Lys Ile Gly Asp Leu Gly Leu Ala Ala Arg Ile Glu Tyr Asp  
165 170 175

Gly Gln Arg Lys Lys Thr Leu Cys Gly Thr Pro Asn Tyr Ile Ala Pro  
180 185 190

Glu Ile Leu Ser Lys Thr Gly His Ser Phe Glu Val Asp Val Trp Ser  
195 200 205

Ile Gly Cys Ile Met Tyr Thr Leu Leu Val Gly Lys Pro Pro Phe Glu  
210 215 220

Thr Asn Ser Leu Lys Glu Thr Tyr Ala Arg Ile Ala Arg Cys Asp Tyr  
225 230 235 240

Ser Leu Pro Pro His Leu Asn Lys Asn Ala Ser Ser Leu Ile Asn Lys  
245 250 255

Met Leu Gln Tyr Asp Pro Lys Lys Arg Pro Cys Val Ser Asp Ile Met  
260 265 270

Lys Ala Asp Phe Phe Thr Thr Gly Tyr Met Pro Lys Lys Leu Pro Pro  
275 280 285

Ser Cys Leu Thr Met Ala Pro Arg Phe Asp Ser Ile Asn Tyr Arg Glu  
290 295 300

Ser Ile Ser Asn Arg Arg Pro Leu Asn Glu Leu Asn Ser Pro Lys Ala  
305 310 315 320

Ala Ile Ile Lys Val Ala Ser Lys Pro Gln Asp Pro Val Asn Lys Leu  
325 330 335

Pro Met Phe Asn Ile Pro Asn Lys Pro Thr Thr Gly Asn Gly Val Ser  
340 345 350

Ser Asn Asp Cys Lys Glu Tyr Met Met Ser Leu Glu Arg Glu Leu Gly  
355 360 365

Asn Leu Leu Lys Cys Lys Pro Thr Met Lys Gly Met Lys Asn Met Glu  
370 375 380

Glu Asn Thr Asp Pro Ala Ala Gln Pro Leu Ile Trp Val Ser Lys Trp  
385 390 395 400

Val Asp Tyr Ser Asp Lys Tyr Gly Phe Gly Tyr Glu Leu Ser Asp Asp  
405 410 415

Cys Val Gly Val Met Phe Asn Asp Phe Thr Arg Ile Val Leu Leu Ala  
420 425 430

Asn Leu Lys Asp Val His Tyr Ile Glu Arg Asn Gly Ser Glu Gln Tyr  
435 440 445

His Thr Thr Glu His Thr Pro Pro Ser Leu Glu Lys Lys Met Lys Leu ,

450

455

460

Leu Met Tyr Phe Arg Arg Tyr Met Asn Asp His Leu Ile Lys Ala Gly

465

470

475

480

Ala Asp Ile Leu Ala Lys Asp Ala Asp Gln Leu Ser Arg Thr Pro Tyr

485

490

495

Met Tyr Gln Trp Tyr Arg Ser Thr Ser Ser Val Ile Met Gln Leu Thr

500

505

510

Asn Gly Thr Leu Gln Ile Asn Phe Thr Asp His Thr Lys Val Ile Leu

515

520

525

Cys Pro Leu Met Asn Ala Val Thr Phe Ile Glu Asn Asn Val Phe Arg

530

535

540

Thr Tyr Arg Phe Asn Thr Ile Ala Glu His Gly Cys Ser Pro Glu Leu

545

550

555

560

Gly Lys Cys Leu Glu Tyr Ala His Lys Lys Ile Gly Ser Ile Leu Lys

565

570

575

Asp Ser Pro Val

580

<210> 3

<211> 1217

<212> DNA

<213> *Aphis gossypii*

<400> 3

gatttcttta ctactgggta tatgcctaaa aaattacctc catcatgtct tacaatggct	60
cctcgttttg attctatcaa ttacagagaa tcaatttcta atcgagacc actcaatgaa	120
ctcaatagcc ccaaagctgc catcattaaa gttgcttcta aacctcaaga tccggttaat	180
aaattgcaa tgtttaatat tccaaataaa ccaactactg gaaatgggtg ttcattcaat	240
gactgtaaag aatacatgat gtcccttgaa agagaattgg gaaatttatt gaaatgtaa	300
ccaacatga aaggaatgaa aaacatggag gaaaacactg acccagctgc tcaacctctc	360
atttgggtta gtaaattgggt ggactattcc gataaatatg gatttggata tgaattatct	420
gatgattgtg ttggtggtat gttcaatgat tttaccagaa tagtactttt agccaatcta	480
aaagatgtcc attacataga aagaaatgggt tcagaacaat accatacaac tgaacatact	540
ccaccgtcgt tagagaaaaa aatgaagtta ttgatgtact tcagacgtta catgaatgat	600
catcttatta aagctgggtg tgatatatta gctaaagatg cagaccaatt gagtcgtaca	660
ccatacatgt accaatggta taggtctact tcatcagtta ttatgcaact tactaacggc	720
actttacaaa tcaacttcac agatcataca aaagtaatat tgtgtccatt aatgaatgct	780
gtcaccttta ttgaaaataa tgttttccgt acataccgtt ttaatacaat tgctgaacat	840
ggctgtagcc ctgaattagg aaaatgcttg gaatatgctc acaagaaaat tggatctata	900
ttaaaagata gccagttta atttacttga aaattgacga gtatatttag tttatagtta	960
tgataattaa tgaaaaacca gtacttatgt taaaagagct atatttaaga ttgtaataa	1020
ttactattat tttttttatt ttacaatatt aatattaaac cttaaaatta aatagtttca	1080
tttattatta tttttattat ttctattttg tgatttttgt tatttagaaa actattatct	1140
catcaaaata aagtgactta agtacattta gttacatatt aaaaaatcta atatgttttt	1200
ccatgggtgc attaaaa	1217

&lt;210&gt; 4

&lt;211&gt; 306

&lt;212&gt; PRT

&lt;213&gt; Aphis gossypii

&lt;400&gt; 4

Asp Phe Phe Thr Thr Gly Tyr Met Pro Lys Lys Leu Pro Pro Ser Cys  
 1 5 10 15

Leu Thr Met Ala Pro Arg Phe Asp Ser Ile Asn Tyr Arg Glu Ser Ile  
 20 25 30

Ser Asn Arg Arg Pro Leu Asn Glu Leu Asn Ser Pro Lys Ala Ala Ile  
 35 40 45

Ile Lys Val Ala Ser Lys Pro Gln Asp Pro Val Asn Lys Leu Pro Met  
 50 55 60

Phe Asn Ile Pro Asn Lys Pro Thr Thr Gly Asn Gly Val Ser Ser Asn  
 65 70 75 80

Asp Cys Lys Glu Tyr Met Met Ser Leu Glu Arg Glu Leu Gly Asn Leu  
 85 90 95

Leu Lys Cys Lys Pro Thr Met Lys Gly Met Lys Asn Met Glu Glu Asn  
 100 105 110

Thr Asp Pro Ala Ala Gln Pro Leu Ile Trp Val Ser Lys Trp Val Asp  
 115 120 125

Tyr Ser Asp Lys Tyr Gly Phe Gly Tyr Glu Leu Ser Asp Asp Cys Val  
 130 135 140



Gly Val Met Phe Asn Asp Phe Thr Arg Ile Val Leu Leu Ala Asn Leu  
145 150 155 160

Lys Asp Val His Tyr Ile Glu Arg Asn Gly Ser Glu Gln Tyr His Thr  
165 170 175

Thr Glu His Thr Pro Pro Ser Leu Glu Lys Lys Met Lys Leu Leu Met  
180 185 190

Tyr Phe Arg Arg Tyr Met Asn Asp His Leu Ile Lys Ala Gly Ala Asp  
195 200 205

Ile Leu Ala Lys Asp Ala Asp Gln Leu Ser Arg Thr Pro Tyr Met Tyr  
210 215 220

Gln Trp Tyr Arg Ser Thr Ser Ser Val Ile Met Gln Leu Thr Asn Gly  
225 230 235 240

Thr Leu Gln Ile Asn Phe Thr Asp His Thr Lys Val Ile Leu Cys Pro  
245 250 255

Leu Met Asn Ala Val Thr Phe Ile Glu Asn Asn Val Phe Arg Thr Tyr  
260 265 270

Arg Phe Asn Thr Ile Ala Glu His Gly Cys Ser Pro Glu Leu Gly Lys  
275 280 285

Cys Leu Glu Tyr Ala His Lys Lys Ile Gly Ser Ile Leu Lys Asp Ser  
290 295 300

Pro Val  
305

<210> 5  
<211> 23  
<212> DNA  
<213> artificial sequence

<220>  
<223> oligonucleotide primer

<400> 5  
cgactggagc acgaggacac tga

23

<210> 6  
<211> 21  
<212> DNA  
<213> artificial sequence

<220>  
<223> oligonucleotide primer

<400> 6  
aatgagaggt tgagcagctg g

21

<210> 7  
<211> 7  
<212> PRT  
<213> artificial sequence

<220>  
<223> peptide

<400> 7

Pro Ala Ala Gln Pro Leu Ile  
1 5

<210> 8  
<211> 23  
<212> DNA

<213> artificial sequence

<220>

<223> oligonucleotide primer

<400> 8

aaagctcctc tgaacgtcgc aac

23

<210> 9

<211> 44

<212> RNA

<213> artificial sequence

<220>

<223> oligonucleotide primer

<400> 9

cgacuggagc acgaggacac ugacauaggac ugaaggagua gaaa

44